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(iii) NUMBER OF SEQUENCES: 6

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(C) CITY: Philadelphia
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(E) COUNTRY: USA
(F) ZIP: 19103-2793

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

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(A) APPLICATION NUMBER:

(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

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(C) REFERENCE/DOCKET NUMBER: GM10127

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(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2201 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TAATTTAAAA AGCAACTATT GTATAGAAAA ATACAAAATT TAAAATATAT TACCTTATTA
60
GAAAAAGTCG TAATATGAGG TGTACAAATG ACGCAAATTT TAATAGTAGA AGATGAACAA
120
AACTTAGCAA GATTTCTTGA ATTGGAACTC ACACATGAAA ATTACAATGT GGACACAGAG
180
TATGATGGAC AAGACGGTTT AGATAAAGCG CTTAGCCATT ACTATGATTT AATCATATTA
240
GATTTAATGT TGCCGTCAAT TAATGGCTTA GAAATTTGTC GCAAAATTAG ACAACAACAA
300
TCTACACCTA TCATTATAAT TACAGCGAAA AGTGATACGT ATGACAAAGT TGCTGGGCTT
360

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GATTACGGTG CAGACGATTA TATAGTTAAG CCGTTTGATA TTGAAGAACT TTTAGCAAGA
420
ATTCGTGCAA TTTTACGTCG TCAGCCACAA AAGGATATTA TCGATGTCAA CGGTATTACA
480
ATTGATAAGA ACGCTTTTAA AGTGACGGTA AATGGCGCAG AAATTGAATT AACAAAAACA
540
GAGTATGATT TACTATATCT TCTAGCTGAA AATAAAAAACC ATGTTATGCA ACGGGAACAA
600
ATTTTAAATC ATGTATGGGG TTATAATAGT GAAGTAGAAA CAAATGTCGT AGATGTTTAT
660
ATAAGATATT TACGAAACAA GTTAAAACCA TACGATCGTG ACAAATGAT TGAAACAGTT
720
CGTGGCGTTG GGTATGTGAT ACGATGACAA AACGTAAATT GCGCAATAAC TGGATTATTG
780
TTACCACGAT GATTACGTTT GTCACGATAT TTTTGTTTTG TTTAATTATT ATTTTTTTCT
840
TGAAAGATAC ACTGCATAAT AGTGAGCTTG ATGATGCAGA ACGAAGCTCA AGCGATATTA
900
ATAATTTATT TCATTCTAAG CCTGTAAAG ATATATCTGC ATTAGACTTG AATGCATCTT
960
TAGGTAATTT TCAAGAGATA ATTATTTATG ATGAGCATAA TAATAAATTA TTTGAGACAT
1020
CGAATGATAA CACAGTGAGA GTTGAACCAG GTTATGAACA CCGTTATTTT GACCGCGTAA
1080
TAAAAAAACG CTATAAAGGC ATTGAATATT TAATTATTAA AGAACCAATT ACAACGCAAG
1140
ATTTCAAAGG GTATAGCTTG TTAATTCATT CACTAGAAAA TTATGATAAC ATCGTAAAT
1200
CATTGTATAT CATTGCGCTG GCATTTGGAG TGATTGCAAC AATTATAACT GCCACAATCA
1260
GTTATGTATT TTCAACACAA ATTACTAAAC CGCTTGTGAG TTTATCAAAT AAAATGATTG
1320
AGATTCGACG AGATGGTTTT CAAAATAAAT TGCAATTAAA TACAAATTAT GAAGAAATAG
1380
ATAATTTAGC AAATACGTTT AATGAGATGA TGAGCCAAAT TGAAGAATCA TTTAATCAAC
1440
AAAGACAATT TGTGGAAGAT GCGTCACATG AATTACGAAC ACCATTACAA ATTATTCAAG
1500
GTCATTTAAA TTTGATTGAG CGATGGGGAA AAAAAGACCC AGCAGTATTA GAAGAATCGT
1560

TAAATATTTT TATTGAAGAA ATGAATCGTA TCATAAAATT AGTCGAAGAA TTACTTGAAT
 1620
 TGAATAAAGG AGATGTAAAT GACATTTCTT CTGAAGCGCA GACCGTGCAT ATTAATGATG
 1680
 AAATTCGCTC GCGAATACAC TCATTAAAAC AATTGCATCC TGATTATCAA TTTGATACGG
 1740
 ATCTGACATC TAAAAATCTA GAAATTAAAA TGAAACCTCA TCAATTTCGAA CAATTATTTT
 1800
 TAATCTTTAT TGATAATGCA ATCAAATATG ATGTGAAGAA TAAGAAAATT AAAGTTAAGA
 1860
 CAAGGTTAAA AAATAAGCAA AAAATAATTG AAATTACAGA TCATGGAATT GGTATTCCAG
 1920
 AGGAAGATCA AGATTTTATT TTTGATCGCT TTTATCGAGT GGATAAATCT CGTTCAAGAA
 1980
 GTCAAGGCGG TAATGGACTC GGATTATCTA TTGCTCAAAA AATCATTCAA TTAAACGGAG
 2040
 GATCGATTAA AATTAAAAAGT GAAATTAATA AAGGAACAAC GTTTAAAAATC ATATTTTAAT
 2100
 CATGTCTGAG ACGTCAATCA AAGTCATAGG ATCAATTTTT TAAGTACACA TTAGCTGTGA
 2160
 CTAATGTATA AGAACAACTA TAAACAAAT AACAGTGGT T
 2201

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Lys	Arg	Lys	Leu	Arg	Asn	Asn	Trp	Ile	Ile	Val	Thr	Thr	Met
1				5					10					15	
Ile	Thr	Phe	Val	Thr	Ile	Phe	Leu	Phe	Cys	Leu	Ile	Ile	Ile	Phe	Phe
			20					25					30		
Leu	Lys	Asp	Thr	Leu	His	Asn	Ser	Glu	Leu	Asp	Asp	Ala	Glu	Arg	Ser
		35					40						45		

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Ser	Ser	Asp	Ile	Asn	Asn	Leu	Phe	His	Ser	Lys	Pro	Val	Lys	Asp	Ile
50						55					60				
Ser	Ala	Leu	Asp	Leu	Asn	Ala	Ser	Leu	Gly	Asn	Phe	Gln	Glu	Ile	Ile
65					70				75					80	
Ile	Tyr	Asp	Glu	His	Asn	Asn	Lys	Leu	Phe	Glu	Thr	Ser	Asn	Asp	Asn
				85				90					95		
Thr	Val	Arg	Val	Glu	Pro	Gly	Tyr	Glu	His	Arg	Tyr	Phe	Asp	Arg	Val
			100				105					110			
Ile	Lys	Lys	Arg	Tyr	Lys	Gly	Ile	Glu	Tyr	Leu	Ile	Ile	Lys	Glu	Pro
		115				120					125				
Ile	Thr	Thr	Gln	Asp	Phe	Lys	Gly	Tyr	Ser	Leu	Leu	Ile	His	Ser	Leu
	130					135				140					
Glu	Asn	Tyr	Asp	Asn	Ile	Val	Lys	Ser	Leu	Tyr	Ile	Ile	Ala	Leu	Ala
145					150				155					160	
Phe	Gly	Val	Ile	Ala	Thr	Ile	Ile	Thr	Ala	Thr	Ile	Ser	Tyr	Val	Phe
				165				170						175	
Ser	Thr	Gln	Ile	Thr	Lys	Pro	Leu	Val	Ser	Leu	Ser	Asn	Lys	Met	Ile
			180					185					190		
Glu	Ile	Arg	Arg	Asp	Gly	Phe	Gln	Asn	Lys	Leu	Gln	Leu	Asn	Thr	Asn
	195					200						205			
Tyr	Glu	Glu	Ile	Asp	Asn	Leu	Ala	Asn	Thr	Phe	Asn	Glu	Met	Met	Ser
	210					215				220					
Gln	Ile	Glu	Glu	Ser	Phe	Asn	Gln	Gln	Arg	Gln	Phe	Val	Glu	Asp	Ala
225					230				235					240	
Ser	His	Glu	Leu	Arg	Thr	Pro	Leu	Gln	Ile	Ile	Gln	Gly	His	Leu	Asn
				245				250						255	
Leu	Ile	Gln	Arg	Trp	Gly	Lys	Lys	Asp	Pro	Ala	Val	Leu	Glu	Glu	Ser
			260				265					270			
Leu	Asn	Ile	Ser	Ile	Glu	Glu	Met	Asn	Arg	Ile	Ile	Lys	Leu	Val	Glu
	275						280					285			
Glu	Leu	Leu	Glu	Leu	Thr	Lys	Gly	Asp	Val	Asn	Asp	Ile	Ser	Ser	Glu
	290					295					300				
Ala	Gln	Thr	Val	His	Ile	Asn	Asp	Glu	Ile	Arg	Ser	Arg	Ile	His	Ser
305					310				315					320	
Leu	Lys	Gln	Leu	His	Pro	Asp	Tyr	Gln	Phe	Asp	Thr	Asp	Leu	Thr	Ser
				325				330					335		
Lys	Asn	Leu	Glu	Ile	Lys	Met	Lys	Pro	His	Gln	Phe	Glu	Gln	Leu	Phe
			340				345					350			
Leu	Ile	Phe	Ile	Asp	Asn	Ala	Ile	Lys	Tyr	Asp	Val	Lys	Asn	Lys	Lys
	355					360					365				

Ile Lys Val Lys Thr Arg Leu Lys Asn Lys Gln Lys Ile Ile Glu Ile
 370 375 380
 Thr Asp His Gly Ile Gly Ile Pro Glu Glu Asp Gln Asp Phe Ile Phe
 385 390 395 400
 Asp Arg Phe Tyr Arg Val Asp Lys Ser Arg Ser Arg Ser Gln Gly Gly
 405 410 415
 Asn Gly Leu Gly Leu Ser Ile Ala Gln Lys Ile Ile Gln Leu Asn Gly
 420 425 430
 Gly Ser Ile Lys Ile Lys Ser Glu Ile Asn Lys Gly Thr Thr Phe Lys
 435 440 445
 Ile Ile Phe
 450

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 736 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATTTACGTTT TGTTCATCGTA TCACATACCC AACGCCACGA ACTGTTTCAA TCATTTTGTG
 60
 ACGATCGTAT GGTTTTAACT TGTTCGTAA ATATCTTATA TAAACATCTA CGACATTTGT
 120
 TTCTACTTCA CTATTATAAC CCCATACATG ATTTAAAATT TGTTCCTGTT GCATAACATG
 180
 GTTTTATTT TCAGCTAGAA GATATAGTAA ATCATACTCT GTTTTGTGA ATTCAATTC
 240
 TGCGCCATTT ACCGTCACCT TAAAAGCGTT CTTATCAATT GTAATACCGT TGACATCGAT
 300
 AATATCCTTT TGTGGCTGAC GACGTAAAAT TGCACGAATT CTTGCTAAAA GTTCTTCAAT
 360
 ATCAAACGGC TTAACATAT AATCGTCTGC ACCGTAATCA AGCCAGCAA CTTTGTGATA
 420
 CGTATCACTT TTCGCTGTAA TTATAATGAT AGGTGTAGAT TGTGTTGTC TAATTTTGCG
 480

ACAAATTTCT AAGCCATTAA TTGACGGCAA CATTAAATCT AATATGATTA AATCATAGTA
540
ATGGCTAAGC GCTTTATCTA AACCGTCTTG TCCATCATAC TCTGTGTCCA CATTGTAATT
600
TTCATGTGTG AGTTCCAATT CAAGAAATCT TGCTAAGTTT TGTTTCATCTT CTACTATTAA
660
AATTTGCGTC ATTTGTACAC CTCATATTAC GACTTTTTCT AATAAGGTAA TATATTTTAA
720
ATTTTGTATT TTTCTA
736

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Thr	Gln	Ile	Leu	Ile	Val	Glu	Asp	Glu	Gln	Asn	Leu	Ala	Arg	Phe
1				5					10					15	
Leu	Glu	Leu	Glu	Leu	Thr	His	Glu	Asn	Tyr	Asn	Val	Asp	Thr	Glu	Tyr
			20					25					30		
Asp	Gly	Gln	Asp	Gly	Leu	Asp	Lys	Ala	Leu	Ser	His	Tyr	Tyr	Asp	Leu
		35				40					45				
Ile	Ile	Leu	Asp	Leu	Met	Leu	Pro	Ser	Ile	Asn	Gly	Leu	Glu	Ile	Cys
		50				55					60				
Arg	Lys	Ile	Arg	Gln	Gln	Gln	Ser	Thr	Pro	Ile	Ile	Ile	Ile	Thr	Ala
65				70					75					80	
Lys	Ser	Asp	Thr	Tyr	Asp	Lys	Val	Ala	Gly	Leu	Asp	Tyr	Gly	Ala	Asp
			85					90					95		
Asp	Tyr	Ile	Val	Lys	Pro	Phe	Asp	Ile	Glu	Glu	Leu	Leu	Ala	Arg	Ile
			100					105					110		
Arg	Ala	Ile	Leu	Arg	Arg	Gln	Pro	Gln	Lys	Asp	Ile	Ile	Asp	Val	Asn
		115				120						125			
Gly	Ile	Thr	Ile	Asp	Lys	Asn	Ala	Phe	Lys	Val	Thr	Val	Asn	Gly	Ala
		130				135						140			

